

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2000, 20:28:05 ; Search time 49.29 Seconds
(without alignments)
385.353 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDCARKQPIKEETEAIEH 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	851.5	25.2	396	P53_SALIR	P25035 salmo irideus
2	801.5	23.7	373	P53_BRARE	P79734 brachydanio
3	778.5	23.0	381	P53_CANFA	Q29537 canis fam1
4	778	23.0	367	P53_CHICK	P10360 gallus gall
5	776	22.9	386	P53_FELCA	P41685 felis silve
6	760.5	22.5	386	P53_BOVIN	Q29628 bos taurus
7	755.5	22.3	382	P53_SHEEP	P51664 ovis aries
8	752	22.2	351	P53_ORYLA	P79820 oryza lat
9	749	22.1	396	P53_MESAU	Q00366 mesocricetu
10	745.5	22.0	393	P53_CRIGR	O09185 cricetus
11	741	21.9	363	P53_XENLA	P07193 xenopus lae
12	735.5	21.7	391	P53_RAT	P10361 rattus norv
13	725.5	21.4	393	P53_MACMU	P58424 macaca mula
14	724.5	21.4	391	P53_RABIT	Q95330 oryctolagus
15	724.5	21.4	393	P53_HUMAN	P04637 homo sapien
16	723.5	21.4	393	P53_MACFA	P56423 macaca fasc
17	718.5	21.2	393	P53_CERAE	P13481 cercopithec
18	711.5	21.0	390	P53_MOUSE	P02340 mus musculus
19	695	20.5	366	P53_PLAFE	O12945 platichthys
20	691.5	20.4	280	P53_HORSE	P79892 equus caball
21	686.5	20.3	314	P53_SPEBE	Q64662 spermophilu
22	600.5	17.7	207	P53_EQUAS	Q29480 equus asinu
23	133	3.9	1273	WEB1_YEAST	P38968 saccharomyc
24	129	3.8	306	EXTN_DAUCA	P06599 daucus caro
25	127.5	3.8	784	SP4_HUMAN	Q02446 homo sapien
26	126	3.7	817	VRP1_YEAST	P37370 saccharomyc
27	124.5	3.7	358	PGCV_MOUSE	Q62059 mus musculus
28	124	3.7	1051	ULK1_MOUSE	O70405 mus musculus
29	123.5	3.6	1618	NEST_HUMAN	P48681 homo sapien
30	123	3.6	1227	LAF4_HUMAN	P51826 homo sapien
31	123	3.6	1638	BRM_DROME	P25439 drosophila
32	123	3.6	2441	CBP_MOUSE	P5481 mus musculus
33	121.5	3.6	1395	IFAG_HUMAN	Q04637 homo sapien
34	119.5	3.5	971	AREA_FUSMO	P78688 fusarium mo

35	119.5	3.5	2458	1	MAPB_HUMAN	P46821 homo sapien
36	118.5	3.5	635	1	VP40_HSV1	P10210 herpes simp
37	118	3.5	1081	1	GALY_YEAST	P19659 saccharomyc
38	118	3.5	1736	1	ZOI_HUMAN	Q07157 homo sapien
39	117	3.5	1321	1	IRS2_MOUSE	P81122 mus musculus
40	116	3.4	620	1	EXTN_TOBAC	P13983 nicotiana t
41	115	3.4	907	1	VGP3_EBV	P03200 Epstein-bar
42	115	3.4	2365	1	FINC_BOVIN	P07589 bos taurus
43	114	3.4	876	1	AREA_EMENI	P17429 emericella
44	114	3.4	1244	1	SLAI_YEAST	P32790 saccharomyc
45	113	3.3	1125	1	Y079_HUMAN	P53992 homo sapien

ALIGNMENTS

RESULT 1
P53_SALIR
ID P53_SALIR STANDARD; PRT; 396 AA.
AC P25035;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSING PROTEIN).
GN TP53.
OS Salmo irideus (Rainbow trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
OC Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92210006.
RA DE FROMENTEL C.C.; PADKEL F.; CHAPUS A.; BANEY C.; MAY P.; SOUSSI T.;
RT "Rainbow trout p53: cDNA cloning and biochemical characterization.";
RL Gene 112:241-245(1992).
CC -!- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION, IT IS A
CC TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION
CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
CC THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; M75145; AAA49605.1;
FIR; JH0631; JH0631.
DR HSSP; P04637; ITR.
DR PROSITE; PS00348; P53; 1.
DR PFAM; PF00870; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 302 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MCD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 396 AA; 43966 MW; BD1FC37 CRC32;

Query Match 25.2%; Score 851.5; DB 1; Length 396;

Best Local Similarity 55.6%; Pred. No. 1.3e-49;

Matches 170; Conservative 43; Mismatches 86; Indels 7; Gaps 5;

QY 93 VPTHSPYQPS-STEDTMS-PAPVPSNTDYPGPHFEVTFQOSAKSATWTYSPLLK 150

b 61 VSATEPAPQPSISTLDGSPPTSTVPTSDYPALGFQFLQSSAKSVCTYSPDLNK 120
y 151 LYCOLAKTCPIQIKVSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDFNGQSAP 210
b 121 LFCQAKTCFQIIVDHPGAVRALAIKKLSADVAVRCPHQSTSENNEG-PAP 179
y 211 ASHLIRVEGNLSQYDVPDVTGROSVVYPPQVGTFTTILYNFMCNSSCGVMNRRP 270
b 180 RGHVVRBGNORSEMEDGNTLRHSLVLPYPPQVGTFTTILYNFMCNSSCGVMNRRP 239
y 271 ILIITLMEGRGOVLGRSEGRICACPGDRKADHDHYREQALN-ESSAKNGAASKRA 329
b 240 ILIITLMEGRGOVLGRSEGRICACPGDRKADHDHYREQALN-ESSAKNGAASKRA 299
y 330 FKQSPVAPPALGAGVKKRRH---GDEDTYYLYVGRGRENFEILMKLESLELMELV 386
b 300 MKEASLPAPQPGASKTKKSPAVSDDEIYTLQIRGKEVEMLKFKFNDSELSLVPVADA 359
y 387 DSYRQO 392
b 360 DRYROK 365

RESULT 2
D P53 BRARE STANDARD; PRT; 373 AA.
C P79734;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 15-DEC-1998 (Rel. 37, Last annotation update)
E CELLULAR TUMOR ANTIGEN P53.
N TP53.
S Brachydanio rerio (Zebrafish) (Zebra danio).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
C Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
C Cyprinidae; Cyprininae; Rasbora; Rasbora; Danio.
P [1]
N SEQUENCE FROM N.A.
X MEDLINE: 97344388.
A CHENG R., FORD B.L., O'NEAL P.E., MATHEWS C.Z., BRADFORD C.S.,
A THONGTAN T., BARNES D.W., HENDRICKS J.D., BAILEY G.S.;
T "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
T expression during embryogenesis."
L Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
C -!- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
C GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
C CIRCUMSTANCES OR CELL TYPE. BUT BOTH ACTIVITIES ARE INVOLVED IN
C TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION, IT IS A
C TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION
C BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
C THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
C APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
C BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
C EXPRESSION (BY SIMILARITY).
C -!- SUBCELLULAR LOCATION: NUCLEAR.
C -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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C EMBL: U60804; AAB40617.1;
C HSP: P04637; I7SR.
C ZFIN: ZDB-GENE-990415-32; TP53.
C PROSITE: PS00348; P53; 1.
C PFAM: PF00870; P53; 1.
C W Anti-oncogene; DNA-binding; Transcription regulation; Activator;
C Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 373 AA; 41899 MW; 706A4B9C CRC32;
Query Match 23.7%; Score 801.5; DB 1; Length 373;
Best Local Similarity 51.0%; Pred. No. 2.9e-46;
Matches 158; Conservative 50; Mismatches 91; Indels 11; Gaps 5;
QY 85 YPEHAASVPTSPHQAQSSFTDMSAPVIPSNTDYPGPHFEVTFQOQSSTAKSATWY 144
DB 41 FPNFENFVLEQP--QPS-----LTPPTSTVPTESDYPGDFRLRFPQSGTAKSVCTY 94
QY 145 SPLLKLLKQCIQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDFN 204
DB 95 SPDLNKLFCQLAKTCFQIIVDHPGAVRALAIKKLSADVAVRCPHQSTSENNEG-PAP 152
QY 205 EGOSAPASHLIRVEGNLSQYDVPDVTGROSVVYPPQVGTFTTILYNFMCNSSCVG 264
DB 153 GDNLPAGHLIRVEGNQRANYREDNITLRHSVFPVYEPALGAEWTVLLNYMCNSSCMG 212
QY 265 GNNRRPILITLMEGRGOVLGRSEGRICACPGDRKADHDHYREQALNNESSAKNGA 324
DB 213 GNNRRPILITLMEGRGOVLGRSEGRICACPGDRKADHDHYREQALNNESSAKNGA 271
QY 325 ASKRAFQKQSPVAPPALGAGVKKRR--HGEDTYYLYVGRGRENFEILMKLESLELMELV 382
DB 272 GTRKSLRVKRESSATLURPEGSKKAKGSSDDEIFTLQVRGRERYEILKLNDSLELSDVVP 331
QY 383 QPLVDSYRQO 392
DB 332 ASDAEKYROK 341

RESULT 3
P53_CANFA
ID P53_CANFA STANDARD; PRT; 381 AA.
AC Q29537;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53.
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LEUKOCYTE;
RX MEDLINE: 98178696.
RA VELDHOFEN N., MILNER J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
RT full length canine p53 protein."
RL Oncogene 16:1077-1084(1998).
RN [2]
RP SEQUENCE OF 25-300 FROM N.A.
RC STRAIN-BEAGLE;
RX MEDLINE: 95323915.
RA KRAEGL S.A., PAZZI K.A., MADEWELL B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8";
RL Cancer Lett. 92:181-186(1995).
CC -!- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE. BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION, IT IS A
CC TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION
CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
CC THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY

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CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; AF060514; AAC16909.1; ..
CC EMBL; S77819; ABA42022.1; ..
CC HSP; P04637; 1YCS.
CC PROSITE; PS00348; P53; 1.
CC PFAM; PF00870; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis.
CC DOMAIN 1 59 ASP/GLU-RICH (ACIDIC).
CC FT DOMAIN 68 137 HYDROPHOBIC.
CC FT DOMAIN 307 381 HIGHLY BASIC AND MAY BE INVOLVED IN
CC FT INTERACTION WITH DNA (BY SIMILARITY).
CC FT DOMAIN 299 311 INTERACTION WITH DNA (BY SIMILARITY).
CC FT MOD_RES 380 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT PHOSPHORYLATION (BY SIMILARITY).
CC SQ SEQUENCE 381 AA; 42486 MW; 70210863 CRC32;

Query Match 23.0%; Score 778.5; DB 1; Length 381;
Best Local Similarity 44.1%; Pred. No. 8.5e-45;
Matches 165; Conservative 57; Mismatches 93; Indels 59; Gaps 8;

QY 14 TFEHLWSLEPDSTYFDLPQSSRGNNVGGTSSMDVFLHGMTTSVMAQFNLLSMD 73
DB 18 TPESELWNL-----LPENNVLSSELCPAVDELL-----LPESVW---NWLDESD 58
QY 74 QMSRAASASPTPEHAASVTHSPYAPQSPSTFTMSAPVPSNTDYPGPHFEVTFQ 133
DB 59 DAPRMPATSAPTAGPAPSWPLSS-----VPSKTPYPTGYFRLGLFLH 102

QY 134 SSTAKSATWTSPLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHVTDVWR 193
DB 103 SGTAKSVTWTSPLNKLFCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHVTDVWR 162
QY 194 CPNHELGRDFNEGOSAPASHIRVEGNLSQYVDVDTGVSQVVPVPEPQVGTETTL 253
DB 163 CPHERCSDSDG-LAPPQHILIRVEGNLRAKYLDRNTRFRSHVVPVPEPVGSDYTTIH 221
QY 254 YNMCNNSCVGMNRRPILIIITLEMGRDGOVGLRRSFEGRICACGRDRKADSDHYREQ 313
DB 222 YNMCNNSCVGMNRRPILIIITLEMGRDGOVGLRRSFEGRICACGRDRKADSDHYREQ 279
QY 314 ALNESSAKNG-----AASKRAFKSPAPVAPGALGVKRRRGDEDTYLLQVGRNF 365
DB 279 -----KKGPCPEPPPGSTKRALPSTSSSP-----OKKPLDGEVFTLQIRGRY 326
QY 366 EILMKLKESLEME 379
DB 327 EMFNLNLEALEKD 340

RESULT 4
P53_CHICK
ID P53_CHICK STANDARD; PRT; 367 AA.
AC P10360;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53.
GN TP53.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPAFAS;
RX MEDLINE; 89083584.
RA SOUSSI T.;
RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
RL oncoprotein"; Res. 16:11383-11383(1989).
CC -1- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION. IT IS A
CC TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION
CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
CC THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; X13057; CAA31456.1; ..
CC PIR; S02193; S02193.
CC HSP; P04637; 1TSR.
CC DR PROSITE; PS00348; P53; 1.
CC DR PFAM; PF00870; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis.
CC FT DOMAIN 289 302 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
CC SQ SEQUENCE 367 AA; 40169 MW; 538569C4 CRC32;

Query Match 23.0%; Score 778; DB 1; Length 367;
Best Local Similarity 44.1%; Pred. No. 8.8e-45;
Matches 164; Conservative 56; Mismatches 106; Indels 46; Gaps 7;

QY 15 FEHLSWSLEPDSTYFDLPQSSRGNNVGGTSSMDVFLHGMTTSVMAQFNLLSMDQ 74
DB 15 FMDLSMLPYSMOQLPDPEDHSNQEL-----SPLP 46
QY 75 MSSRAASASPTPEHAASVTHSPYAPQSPSTFTMSAPVPSNTDYPGPHFEVTFQ 134
DB 47 SDPPPPPPPPPLFLAAAPPLNPTTPRA-----APSPVVPSTEDYGDGDFRQV 101
QY 135 STAKSATWTSPLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHVTDVWR 194
DB 102 GTAKSVTCTSPVLNRYCYELAKPCPVQVGVAPVAPSSSLAVAVYKSEHVEVRR 161
QY 195 PNHELGRDFNEGOSAPASHIRVEGNLSQYVDVDTGVSQVVPVPEPQVGTETTL 254
DB 162 PHHERCGGTDG-LAPAQHLIRVEGNPQARYHDDTTKRSHVVPVPEPVGSDCTTV 220
QY 255 NEMCNNSCVGMNRRPILIIITLEMGRDGOVGLRRSFEGRICACGRDRKADSDHYREQ 314
DB 221 NEMCNNSCVGMNRRPILIIITLEMGRDGOVGLRRSFEGRICACGRDRKADSDHYREQ 280
QY 315 LNESSAKNGAASKRAFKQSPAPVAPGALGVKRRRGDEDTYLLQVGRNFELMKL 374
DB 281 A-----GVAKRA--MSPP-TEAPEPKKRVLPNDNEIFYLQVGRRRRVEMLKE 330
QY 375 LELME--LYPQP 384
DB 331 LQAEAGSAPRP 342
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SULT 5
3_FELCA STANDARD; PRT; 386 AA.
P41865;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CELLULAR TUMOR ANTIGEN P53.
TP53.
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
[1]
SEQUENCE FROM N.A.
TISSUE=LYMPH NODE;
MEDLINE; 94333960.
OKUDA M., UMEDA A., SAKAI T., OHASHI T., MOMOI Y., YOUN H.Y.,
WATARI T., GOITSUKA R., TSUJIMOTO H., HASEGAWA A.,
"Cloning of feline p53 tumor-suppressor gene and its aberration in
hematopoietic tumors.",
Int. J. Cancer 58:602-607(1994).
[2]
SEQUENCE OF 34-354 FROM N.A.
MEDLINE; 94114699.
OKUDA M., UMEDA A., MATSUMOTO Y., MOMOI Y., WATARI T., GOITSUKA R.,
O'BRIEN S.J., TSUJIMOTO H., HASEGAWA A.,
"Molecular cloning and chromosomal mapping of feline p53 tumor
suppressor gene.",
J. Vet. Med. Sci. 55:801-805(1993).
-!- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION, IT IS A
TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION
BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
EXPRESSION.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
IN MANY TYPES OF CANCER.
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; D26608; BAA05653.1;
EMBL; D16460; BAA03927.1;
HSSP; P04637; 1SAH.
PROSITE; PS00348; P53; 1.
PFAM; PF00870; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator;
Nuclear protein; Phosphorylation; Apoptosis.
DOMAIN 1 59 ASP/GLU-RICH (ACIDIC)
DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
CONFLICT 285 285 K -> R (IN REF. 2).
SEQUENCE 386 AA; 42692 MW; D6C7132A CRC32;

Query Match 22.98; Score 776; DB 1; Length 386;
Best Local Similarity 44.48; Pred. No. 1.3e-44;
Matches 170; Conservative 55; Mismatches 104; Indels 54; Gaps 9;
5 TATSPDGGTTTFELHWSLEPSTYFDLPQSSRGNNVGGTSSMDVFLHGGTTSMVAQ 64

Db 9 TIEPPLSQETFSLWNL-----LPE-----NNVLSSELSSAMNLPSEDVA----- 51
QY 65 FNLLSSTMDQMSRAASAPSYTPEHAASVPHSAQSSSTFTDMSAPVTPSNTDYPGP 124
Db 51 -NWLDEAPDDASGMSAVPAPAPATPAPAIS---WPLSSF-----VPSOKTYPGA 98
QY 125 HFEVTFQSSSTAKSATWTYSPLLLKLCQIAKTCPIQIKVSTPPPGTAIRAMPYVYKKA 184
Db 99 YGFHLGFLOGSTAKSVTCYSPPLNKLFCQLAKTCVQLWVRSPPPGTCVRAAIYKKS 158
QY 185 EHYTDVVKCPNHELGRDNFEGSQAPASHLIRVEGNNSQYVDDVPTGRQSVVYVPEPQ 244
Db 159 EFMTYVRRCPHRCPSDDG-LAPPQHLIRVEGNLHAKYLDNRNTRHSHVYVPEPPE 217
QY 245 VGTEFTILYFNMCNSSCVGGMNRRPIIITLEMRDQVLGRSFEGRICACPGRDKA 304
Db 218 VGSDCITIHVFNMCNSSCMGNNRRPIIITLEDNSKLLGRNSFEVRCACPGRDRT 277
QY 305 DEDHYREQALNESSAKNG-----AASKRAFKQSPNVPALGAGVKKRRHGDDETY 356
Db 278 EENFR-----KGEPCPEPPPGSTKRALPPSTSTPP-----QKKKPLDGEYFT 322
QY 357 LQVRGRENFEILMKLESLELME 379
Db 323 LQIRGRERFEMPRLNEALELAD 345

RESULT 6
P53_BOVIN STANDARD; PRT; 386 AA.
ID Q29628;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53.
GN TP53.
OS Bos taurus (Bovine), and Bos indicus (zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=BOVINE; TISSUE=LIVER;
RX MEDLINE; 95352829.
RA DEQUITET F., KETTMANN R., BURNY A., WILLEMS L.;
RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
RL DNA Seq. 5:261-264(1995).
RN [2]
RP SEQUENCE OF 13-386 FROM N.A.
RC SPECIES=BOVINE; STRAIN=HOLSTEIN; TISSUE=THYMUS;
RX MEDLINE; 96401400.
RA KOMORI H., ISHIGURO N., HORIUCHI M., SHINAGAWA M., AIDA Y.;
RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
RL Vet. Immunol. Immunopathol. 52:53-63(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.INDICUS; STRAIN=BORAN; TISSUE=BLOOD;
RA BISHOP R.R.P., GOBRIGHT E.E.I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION, IT IS A
TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION
BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
EXPRESSION.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED

SO SEQUENCE 396 AA; 43631 MW; C2668ADE CRC32;

Query Match 22.1%; Score 749; DB 1; Length 396;
Best Local Similarity 43.9%; Pred. No. 8.1e-43;
Matches 163; Conservative 58; Mismatches 104; Indels 50; Gaps 10;

QY 14 TFEHLWSSLEPDSTYFDLPQSSRGNNVGVGDDSSMDVDFHLEGMTTSVMAQFNLLSSTMD 73
DB 18 TFDLWKLPPNNVLTSPSS-----DSIEELFSENVA-----GWLEDPGE 59

QY 74 QMSRAASASPYTPEHAASVP-----THSPAQSSTFTDMSAPV---IPSNYDYPGPHF 127
DB 60 ALQSGAAAAPAP--AAEDPVAETPAPVASAPAT-----PWPLSSVPSYKTYQDYG 112

QY 128 EVTFQSSAKSATWYSPLLKLYCOIAKTCPIQIKVSTPPPGTATRAMPVYKKAHV 187
DB 113 RLGLHSGTAKSVCTYISPLNKLFCQLAKTCVQVWSSSTPPGTRVRAAIYKLLQIM 172

QY 188 TDVVKCPNHELGRDNFEGOS-APASHLIRVEGNLSQYVDDPVYTGROSVVYPPQVG 246
DB 173 TEVVRCPHERS---SEGDLAPPQHLIRVEGNMHAELDDKQTFRHSVVVYPPPEVG 229

QY 247 TEFTLYNFMNCSSCVGMNRRPILITILEMRDQVLRGSRFEGRICACPRDRKADE 306
DB 230 SDCITTHYNCSSCMGMNRRPILITITLEDPSGNLLGRNSFEVIRACPRDRRTEE 289

QY 307 DHYREQ---QALNESSAKNGAKRAFPQSPAPVAPALGAGVKRRHGDETYVLQVRGR 362
DB 290 KNFQKGEPCPELPKPSAKRALPTNTSSSPQ-----KKTLGDEYFLKIRGO 338

QY 363 ENFEILMKLESLEME 379
DB 339 ERKMFQELNEALEKD 355

RESULT 10

P53_CRIGR STANDARD; PRT; 393 AA.

AC 009185; Q64397; P97258; P97788;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53.

GN TP53 OR P53.
OS Crictetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
RN [1]
RP SEQUENCE FROM N.A.
RA CHAUNG W., MI L.J., BOORSTEIN R.J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 97183659.
RA LEE H., LARNER J.M., HAMLIN J.L.;
RT "Cloning and characterization of Chinese hamster p53 cDNA."
RL Gene 184:177-183(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYONIC FIBROBLAST;
RA SHIMIZU T., NIKAIKO O., SUZUKI F.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION, IT IS A
CC TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION
CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
CC THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2

CC EXPRESSION
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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- RA BENCHIMOL S.;
RT "Isolation and characterization of a human p53 cDNA clone: expression
of the human p53 gene.";
RL EMBO J. 3:3257-3262(1984).
RN [7]
RP NUCLEAR LOCALIZATION SIGNAL.
RX MEDLINE; 90191730.
RA ADDISON C., JENKINS J.R., STURZBECHER H.-W.;
RT "The p53 nuclear localisation signal is structurally linked to a
p34cdc2 kinase motif.";
RL Oncogene 5:423-426(1990).
RN [8]
RP PHOSPHORYLATION BY P60/CDC2 AND CYCLIN B/CDC2.
RX MEDLINE; 90280456.
RA BISCHOFF J.R., FRIEDMAN P.N., MARSHAK D.R., PRIVES C., BEACH D.;
RT "Human p53 is phosphorylated by p60-cdc2 and cyclin B-cdc2.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:4766-4770(1990).
RN [9]
RP DEPHOSPHORYLATION BY PP2A.
RX MEDLINE; 91172186.
RA SCHEIDTMANN K.H., MUMBY M.C., RUNDELL K., WALTER G.;
RT "Dephosphorylation of simian virus 40 large-T antigen and p53 protein
by protein phosphatase 2A: inhibition by small-t antigen.";
RL Mol. Cell. Biol. 11:1996-2003(1991).
RN [10]
RP STRUCTURE BY NMR OF 319-360.
RX MEDLINE; 94294808.
RA CLORE G.M., OWICHINSKI J.G., SAKAGUCHI K., ZAMBRANO N., SAKAMOTO H.,
RA APPELLA E., GROENENBORN A.M.;
RT "High-resolution structure of the oligomerization domain of p53 by
multidimensional NMR.";
RL Science 265:386-391(1994).
RN [11]
RP STRUCTURE BY NMR OF 325-355.
RX MEDLINE; 95292092.
RA LEE W., HARVEY T.S., YIN Y., YAU P., LITCHFIELD D., ARROWSMITH C.H.;
RT "Solution structure of the tetrameric minimum transforming domain of
p53.";
RL Nat. Struct. Biol. 1:877-890(1994).
RN [12]
RP STRUCTURE BY NMR OF 326-354.
RX MEDLINE; 98026899.
RA MCCOY M., STAVRIDIS E.S., WATERMAN J.L., WIECZOREK A.M., OPELLA S.J.,
RA HALAZONETIS T.D.;
RT "Hydrophobic side-chain size is a determinant of the
three-dimensional structure of the p53 oligomerization domain.";
RL EMBO J. 16:6230-6236(1997).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 94-289.
RX MEDLINE; 94294806.
RA CHO Y., GORINA S., JEFFREY P.D., PAVLETICH N.P.;
RT "Crystal structure of a p53 tumor suppressor-DNA complex:
understanding tumorigenic mutations.";
RL Science 265:346-353(1994).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 13-29 IN COMPLEX WITH MDM2.
RX MEDLINE; 97081050.
RA KUSSIE P.H., GORINA S., MARECHAL V., ELENAAS B., MOREAU J.,
RA LEVINE A.J., PAVLETICH N.P.;
RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
transactivation domain.";
RL Science 274:948-953(1996).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 97-287 IN COMPLEX WITH 53BP2.
RX MEDLINE; 97035414.
RA GORINA S., PAVLETICH N.P.;
RT "Structure of the p53 tumor suppressor bound to the ankyrin and SH3
domains of 53BP2.";
RL Science 274:1001-1005(1996).
RN [16]
RP REVIEW.
RX MEDLINE; 94090335.
RA HARRIS C.C.;
RT "p53: at the crossroads of molecular carcinogenesis and risk
assessment.";
RL Science 262:1980-1981(1993).
RN [17]
RP REVIEW ON VARIANTS.
RX MEDLINE; 91289156.
RA HOOLSTEIN M., SIDRANSKY D., VOGELSTEIN B., HARRIS C.C.;
RT "p53 mutations in human cancers.";
RL Science 253:49-53(1991).
RN [18]
RP REVIEW ON VARIANTS.
RX MEDLINE; 96271983.
RA DE VRIES E.M.G., RICKE D.O., DE VRIES T.N., HARTMANN A., BLASZYK H.,
RA LIAO D., SOUSSI T., KOVACH J.S., SOMMER S.S.;
RT "Database of mutations in the p53 and APC tumor suppressor genes
designed to facilitate molecular epidemiological analyses.";
RL Hum. Mutat. 7:202-213(1996).
RN [19]
RP VARIANT ARG-72.
RX MEDLINE; 91153807.
RA OLSCHWANG S., LAURENT-PUIG P., VASSAL A., SALMON R.-J., THOMAS G.;
RT "Characterization of a frequent polymorphism in the coding sequence
of the p53 gene in colonic cancer patients and a control
population.";
RL Hum. Genet. 86:369-370(1991).
RN [20]
RP VARIANT LFS THR-133.
RX MEDLINE; 92034774.
RA LAW J.C., STRONG L.C., CHIDAMBARAM A., FERRELL R.E.;
RT "A germ line mutation in exon 5 of the p53 gene in an extended cancer
family.";
RL Cancer Res. 51:6385-6387(1991).
RN [21]
RP VARIANTS LFS CYS-245; TRP-248; PRO-252 AND LYS-258.
RX MEDLINE; 91057657.
RA MALKIN D., LI F.P., STRONG L.C., FRAUMENI J.F. JR., NELSON C.E.,
RA KIM D.H., KASSEL J., GRYKA M.A., BISCHOFF F.Z., TAINSKY M.A.,
RA FRIEND S.H.;
RT "Germ line p53 mutations in a familial syndrome of breast cancer,
sarcomas, and other neoplasms.";
RL Science 250:1233-1238(1990).
RN [22]
RP VARIANT LFS ASP-245.
RX MEDLINE; 91060929.
RA SRIVASTAVA S., ZOU Z., PIROLLO K., BLATTNER W., CHANG E.H.;
RT "Germ-line transmission of a mutated p53 gene in a cancer-prone
family with Li-Fraumeni syndrome.";
RL Nature 348:747-749(1990).
RN [23]
RP VARIANT LFS LEU-272.
RX MEDLINE; 92147863.
RA FELIX C.A., NAU M.M., TAKAHASHI T., MITSUDOMI T., CHIBA I.,
RA POPLACK D.G., REAMAN G.H., COLE D.E., LETTERIO J.J., WHANG-PENG J.,
RA KNUTSEN T., MINNA J.D.;
RT "Hereditary and acquired p53 gene mutations in childhood acute
lymphoblastic leukemia.";
RL J. Clin. Invest. 89:640-647(1992).
RN [24]
RP VARIANTS LFS HIS-273 AND VAL-325.
RX MEDLINE; 92228023.
RA MALKIN D., JOLLY K.W., BARBIER N., LOOK A.T., FRIEND S.H.,
RA GEBHARDT M.C., ANDERSEN T.I., BORRESSEN A.-L., LI F.P., GARBER J.,
RA STRONG L.C.;
RT "Germline mutations of the p53 tumor-suppressor gene in children and
young adults with second malignant neoplasms.";
RL New Engl. J. Med. 326:1309-1315(1992).
RN [25]
RP VARIANTS BREAST TUMORS GLN-132; SER-249; LYS-280 AND LYS-285.
RX MEDLINE; 90295284.
RA BARTEK J., IGGO R., GANNON J., LANE D.P.;
RT "Genetic and immunochemical analysis of mutant p53 in human breast
cancer cell lines.";
RL Oncogene 5:893-899(1990).

[26]
VARIANTS COLON TUMORS PHE-241 AND HIS-273.
MEDLINE: 91017544.
RODRIGUES N.R., ROWAN A., SMITH M.E.F., KERR I.B., BODMER W.F.,
CANNON J.V., LANE D.P.;
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